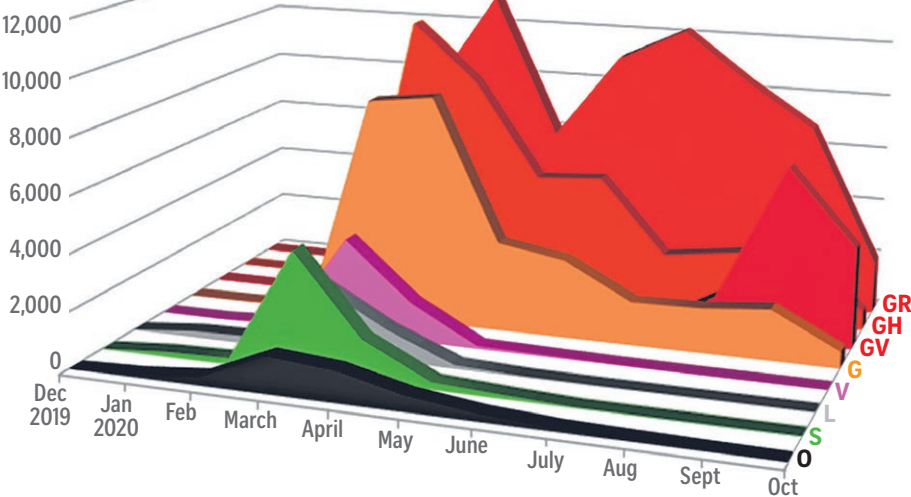


Mutations of the virus during the Covid-19 pandemic

The Sars-CoV-2 virus has mutated into various clades, or branches, during the pandemic. By sequencing the genome of the virus taken from people infected, scientists are able to know if a particular clade is spreading or has been contained.

GLOBAL

Number of virus genomes



Clades:

G - From China, this caused the major wave in Europe, replacing clade V

V - Close relative of clade L was part of outbreak in northern Italy and other parts of Europe

L - This clade stemmed from the main outbreak in Wuhan

S - From southern China. Also in Washington state in the US and in Spain in the early part of pandemic

O - Refers to all other clades

Subclades

(did not start in China, but some of these clades have found their way there):

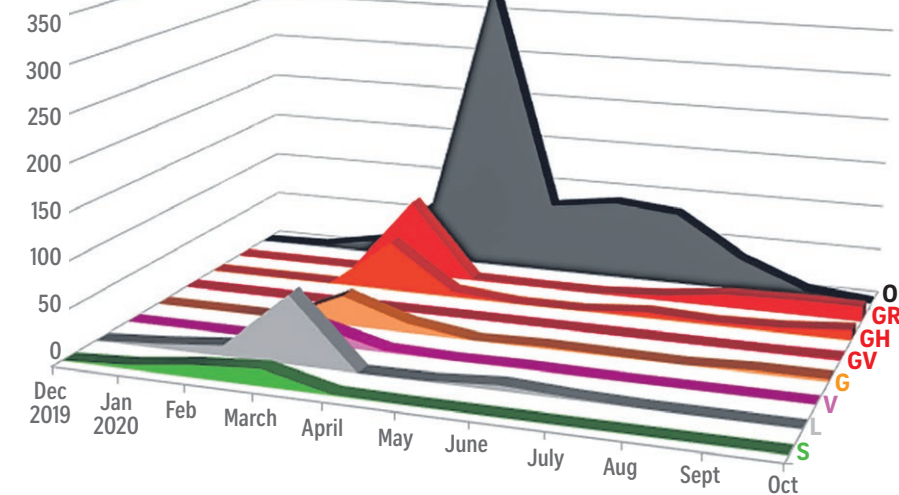
GR - Dominant in Europe

GH - Largely in the US

GV - Spread from Spain to several other European countries

SINGAPORE

Number of virus genomes



Clades:

O - Dormitory clusters

GR, GH, GV - Imported cases on stay-home notice

G - Includes the D614G mutation which is more infectious but not more serious

V - This clade may have come from China or Europe

L - Includes Yong Thai Hang health products shop and Grand Hyatt cluster

S - Includes Grace Assembly of God, The Life Church and Missions Singapore, Science Park II and Seletar Aerospace Heights construction site clusters

NOTE: The letters denoting the clades reflect the key mutation positions on the virus